

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/910,185

DATE: 08/02/2001  
TIME: 10:56:08

Input Set : A:\RTS-0258 Sequence Listing.txt  
Output Set: N:\CRF3\08022001\I910185.raw

6 <110> APPLICANT: C. Frank Bennett  
7 Susan M. Freier  
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3

## EXPRESSION

11 <130> FILE REFERENCE: RTS-0258  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/910,185  
C--> 13 <141> CURRENT FILING DATE: 2001-07-18  
13 <160> NUMBER OF SEQ ID NOS: 90  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 20  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
21 <220> FEATURE:  
23 <223> OTHER INFORMATION: Antisense Oligonucleotide  
25 <400> SEQUENCE: 1 20  
26 tccgtcatcg ctccctcaggg  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 20  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
34 <220> FEATURE:  
36 <223> OTHER INFORMATION: Antisense Oligonucleotide  
38 <400> SEQUENCE: 2 20  
39 atgcattctg cccccaagga  
42 <210> SEQ ID NO: 3  
43 <211> LENGTH: 5055  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Homo sapiens  
47. ~~<220> FEATURE.~~  
49 <220> FEATURE:  
50 <221> NAME/KEY: CDS  
51 <222> LOCATION: (55)...(4845)  
53 <400> SEQUENCE: 3  
54 cgatactacg tggcatttt tggtcgaaga gagctgaagt aatgagaaga catc atg 57  
Met  
55 1  
56  
58 gag gcc cag tcc cac agc tcc acg acc act gaa aag aaa aag gtt gag 105  
59 Glu Ala Gln Ser His Ser Ser Thr Thr Glu Lys Lys Lys Val Glu  
60 5 10 15  
62 aat tcc ata gtg aag tgc tcc act cga aca gat gtg agc gag aaa gcc 153  
63 Asn Ser Ile Val Lys Cys Ser Thr Arg Thr Asp Val Ser Glu Lys Ala  
64 20 25 30  
66 gtt gcc tcc agc acc act tct aat gag gat gaa agt cct gga cag act 201  
67 Val Ala Ser Ser Thr Ser Asn Glu Asp Glu Ser Pro Gly Gln Thr  
68 35 40 45  
70 tat cac aga gag aga aga aac gca atc act atg cag cca cag aat gtc 249  
71 Tyr His Arg Glu Arg Arg Asn Ala Ile Thr Met Gln Pro Gln Asn Val  
72 50 55 60 65

Does Not Comply  
Corrected Diskette Needed

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74	cag	ggg	ctc	agc	aaa	gtc	agt	gag	gaa	cct	tca	aca	tcg	agt	gac	gag	297
75	Gln	Gly	Leu	Ser	Lys	Val	Ser	Glu	Glu	Pro	Ser	Thr	Ser	Ser	Asp	Glu	
76						70			75						80		
78	agg	gcc	tca	ttg	atc	aag	aaa	gag	atc	cat	ggg	tcc	ctg	cca	cac	gtg	345
79	Arg	Ala	Ser	Leu	Ile	Lys	Lys	Glu	Ile	His	Gly	Ser	Leu	Pro	His	Val	
80						85			90						95		
82	gct	gag	ccc	tct	gtg	ccg	tac	cgc	ggg	acg	gtg	ttt	gcc	atg	gac	ccc	393
83	Ala	Glu	Pro	Ser	Val	Pro	Tyr	Arg	Gly	Thr	Val	Phe	Ala	Met	Asp	Pro	
84						100			105						110		
86	agg	aat	gtt	tac	atg	gag	ccc	cac	tac	cac	cct	cct	cat	ttt	ttc	cct	441
87	Arg	Asn	Gly	Tyr	Met	Glu	Pro	His	Tyr	His	Pro	Pro	His	Leu	Phe	Pro	
88						115			120						125		
90	gcc	ttc	cat	cct	cct	gtt	cca	att	gat	gcc	aga	cat	cat	gag	ggc	cgf	489
91	Ala	Phe	His	Pro	Pro	Val	Pro	Ile	Asp	Ala	Arg	His	His	Glu	Gly	Arg	
92	130					135			140						145		
94	tac	cat	tac	gat	cca	tct	ccg	att	cct	cca	ttg	cat	atg	act	tcc	gcc	537
95	Tyr	His	Tyr	Asp	Pro	Ser	Pro	Ile	Pro	Pro	Leu	His	Met	Thr	Ser	Ala	
96						150			155						160		
98	tta	tct	agt	agc	cct	acg	tat	ccg	gac	ctg	ccc	tcc	att	agg	atc	tcc	585
99	Leu	Ser	Ser	Pro	Thr	Tyr	Pro	Asp	Leu	Pro	Phe	Ile	Arg	Ile	Ser		
100						165			170						175		
102	cca	cac	cg	aa	cc	g	ct	g	ct	tcc	gag	tct	ccc	atc	cct	cca	633
103	Pro	His	Arg	Asn	Pro	Ala	Ala	Ser	Glu	Ser	Pro	Phe	Ser	Pro	Pro		
104						180			185						190		
106	cat	ccc	tac	att	aat	ccc	tac	atg	gac	tat	atc	cgc	tcc	ttg	cac	agc	681
107	His	Pro	Tyr	Ile	Asn	Pro	Tyr	Met	Asp	Tyr	Ile	Arg	Ser	Leu	His	Ser	
108						195			200						205		
110	agc	cca	tcg	ctc	tcc	atg	atc	tca	gca	acc	cgt	ggg	ctg	agc	cct	aca	729
111	Ser	Pro	Ser	Leu	Ser	Met	Ile	Ser	Ala	Thr	Arg	Gly	Leu	Ser	Pro	Thr	
112	210					215			220						225		
114	gat	gct	ccc	cat	gca	gga	gtc	agc	cca	gca	gaa	tac	tat	cat	cag	atg	777
115	Asp	Ala	Pro	His	Ala	Gly	Val	Ser	Pro	Ala	Glu	Tyr	Tyr	His	Gln	Met	
116						230			235						240		
118	gcc	ctg	cta	act	ggc	cag	cg	agc	ccc	tat	gca	gac	att	att	ccc	tca	
119	Ala	Leu	Leu	Thr	Gly	Gln	Arg	Ser	Pro	Tyr	Ala	Asp	Ile	Ile	Pro	Ser	
120						245			250						255		
122	gct	gcc	acc	ggc	ggc	acg	ggg	gcc	atc	cac	atg	gaa	tat	ctt	cat	gct	873
123	Ala	Ala	Thr	Ala	Gly	Thr	Gly	Ala	Ile	His	Met	Glu	Tyr	Leu	His	Ala	
124						260			265						270		
126	atg	gat	agc	acc	aga	ttc	tcc	agc	ccc	agg	ctg	tca	gcc	agg	ccg	agc	921
127	Met	Asp	Ser	Thr	Arg	Phe	Ser	Ser	Pro	Arg	Leu	Ser	Ala	Arg	Pro	Ser	
128						275			280						285		
130	cga	aaa	cgt	aca	ctg	tcc	ata	tca	cca	ctc	tcc	gat	cat	agc	ttt	gac	969
131	Arg	Lys	Arg	Thr	Leu	Ser	Ile	Ser	Pro	Leu	Ser	Asp	His	Ser	Phe	Asp	
132	290					295			300						305		
134	ctt	cag	acc	atg	ata	agg	acg	tct	ccc	aac	tcc	ttg	gtc	acg	att	ctc	1017
135	Leu	Gln	Thr	Met	Ile	Arg	Thr	Ser	Pro	Asn	Ser	Leu	Val	Thr	Ile	Leu	
136						310			315						320		
138	aat	aat	tcc	cgt	agc	agc	tct	tca	gca	agt	ggc	tcc	tat	ggt	cac	tta	1065

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139	Asn	Asn	Ser	Arg	Ser	Ser	Ser	Ala	Ser	Gly	Ser	Tyr	Gly	His	Leu
140				325				330				335			
142	tct	gca	agt	gca	atc	agc	cct	gcc	ttg	agc	ttc	acc	tac	tct	tcc
143	Ser	Ala	Ser	Ala	Ile	Ser	Pro	Ala	Leu	Ser	Phe	Thr	Tyr	Ser	Ser
144					340				345			350			
146	ccc	gtc	tct	ctc	cac	atg	cat	cag	cag	atc	cta	agc	cga	caa	cag
147	Pro	Val	Ser	Leu	His	Met	His	Gln	Gln	Ile	Leu	Ser	Arg	Gln	Gln
148						355		360			365				
150	tta	ggt	tca	gcc	ttt	gga	cac	agc	cct	cca	ctc	atc	cac	cct	gcc
151	Leu	Gly	Ser	Ala	Phe	Gly	His	Ser	Pro	Pro	Leu	Ile	His	Pro	Ala
152	370						375			380			385		
154	act	ttt	cca	aca	cag	agg	cct	att	cca	ggg	atc	cct	acg	gtt	ctg
155	Thr	Phe	Pro	Thr	Gln	Arg	Pro	Ile	Pro	Gly	Ile	Pro	Thr	Val	Leu
156						390			395			400			
158	ccc	gtc	cag	gtc	agc	tcc	ggc	cct	tct	gag	tcc	tca	cag	aac	aag
159	Pro	Val	Gln	Val	Ser	Ser	Gly	Pro	Ser	Glu	Ser	Ser	Gln	Asn	Lys
160						405			410			415			
162	acg	agt	gag	tct	gca	gtg	agc	agc	act	ggt	gac	ccg	atg	cac	aag
163	Thr	Ser	Glu	Ser	Ala	Val	Ser	Ser	Thr	Gly	Asp	Pro	Met	His	Asn
164						420			425			430			
166	agg	tcc	aag	atc	aaa	ccc	gat	gaa	gac	ctc	ccc	agc	cca	ggg	gct
167	Arg	Ser	Lys	Ile	Lys	Pro	Asp	Glu	Asp	Leu	Pro	Ser	Pro	Gly	Ala
168						435		440			445				
170	ggg	cag	cag	gaa	cag	ccc	gaa	gga	aca	acc	ctt	gtc	aag	gag	gaa
171	Gly	Gln	Gln	Glu	Gln	Pro	Glu	Gly	Thr	Thr	Leu	Val	Lys	Glu	Gly
172	450						455			460			465		
174	gac	aaa	gat	gaa	agc	aaa	cag	gag	cct	gaa	gtc	atc	tat	gag	aca
175	Asp	Lys	Asp	Glu	Ser	Lys	Gln	Glu	Pro	Glu	Val	Ile	Tyr	Glu	Thr
176							470			475			480		
178	tgc	cac	tgg	gaa	ggc	tgc	gcg	agg	gag	ttc	gac	acc	caa	gag	cag
179	Cys	His	Trp	Glu	Gly	Cys	Ala	Arg	Glu	Phe	Asp	Thr	Gln	Glu	Gln
180						485			490			495			
182	gtg	cac	cat	ata	aat	aac	gac	cat	att	cat	gga	gag	aag	aag	gag
183	Val	His	His	Ile	Asn	Asn	Asp	His	Ile	His	Gly	Glu	Lys	Glu	Phe
184						500			505			510			
186	gtg	tgc	agg	tgg	ctg	gac	tgc	tca	aga	gag	cag	aaa	ccc	ttc	aaa
187	Val	Cys	Arg	Trp	Leu	Asp	Cys	Ser	Arg	Glu	Gln	Lys	Pro	Phe	Lys
188						515		520			525				
190	cag	tat	atg	ttg	gtt	gtg	cat	atg	aga	cac	acg	ggc	gag	aag	cct
191	Gln	Tyr	Met	Leu	Val	Val	His	Met	Arg	Arg	His	Thr	Gly	Glu	Lys
192	530						535			540			545		
194	cac	aaa	tgc	act	ttt	gaa	ggt	tgc	aca	aag	gcc	tac	tcg	aga	cta
195	His	Lys	Cys	Thr	Phe	Glu	Gly	Cys	Thr	Lys	Ala	Tyr	Ser	Arg	Leu
196						550			555			560			
198	aac	ttg	aaa	aca	cac	ttg	aga	gag	aaa	cca	tac	gtc			
199	Asn	Leu	Lys	Thr	His	Leu	Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr
200						565			570			575			
202	tgt	gag	cac	gaa	ggt	tgc	aac	aag	gct	ttc	tca	aat	gcc	tct	gat
203	Cys	Glu	His	Glu	Gly	Cys	Asn	Lys	Ala	Phe	Ser	Asn	Ala	Ser	Asp

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204	580	585	590					
206	gcc	aaa cac caa aac aga acg	cat tcc aat gag	aaa cca tat gtg tgc	1881			
207	Ala	Lys His	Gln Asn Arg	Thr His Ser Asn Glu	Lys Pro Tyr Val Cys			
208	595	600	605		1929			
210	aaa atc	cca ggc tgc	act aag cgt tac aca	gac cca agc tcc ctc	cg			
211	Lys Ile	Pro Gly	Cys Thr Lys Arg	Tyr Thr Asp Pro Ser	Ser Leu Arg			
212	610	615	620	625				
214	aaa cat	gtg aag aca	gtg cat ggc cca	qag gct cat gtc	acc aag aag			
215	Lys His	Val Lys	Thr Val His	Gly Pro Glu Ala	His Val Thr Lys			
216	630	635	640	645				
218	cag cga	ggg gac atc	cat cct cgg	cca ccc ccc	aga gat tcc ggc	2025		
219	Gln Arg	Gly Asp	Ile His	Pro Arg Pro Pro	Arg Asp Ser Gly			
220	645	650	655	660				
222	agc cat	tca cag	tcc agg	tcg cct	ggc cga ccg	act cag gga	gcc ctt	2073
223	Ser His	Ser Gln	Arg Ser	Pro Gly Arg Pro	Thr Gln	Gly Ala	Leu	
224	660	665	670	675	680	685		
226	ggt gag	cag cag	gac ctc	agc aac	act acc tca	aag cgg gaa	gaa tgc	
227	Gly Glu	Gln Gln	Asp Leu	Ser Asn	Thr Thr Ser	Lys Arg Glu	Glu Cys	
228	690	695	700	705	710	715	720	
230	ctc cag	gtg aaa	acc gtc	aag gca	gag aag cca	atg aca	tct cag cca	
231	Leu Gln	Val Lys	Thr Val	Lys Ala	Glu Lys	Pro Met	Thr Ser Gln Pro	
232	690	695	700	705	710	715	720	
234	agc cct	ggt ggt	cag tct	tca tgc	agc agc caa	cag tcc ccc	atc agc	
235	Ser Pro	Gly Gly	Gln Ser	Ser Cys	Ser Gln	Gln Ser Pro	Ile Ser	
236	710	715	720	725	730	735		
238	aac tat	tcc aac	agt ggg	ctc gag	ctt cct	ctg acc	gat gga	ggt agt
239	Asn Tyr	Ser Asn	Ser Gly	Leu Glu	Leu Pro	Leu Thr	Asp Gly	Gly Ser
240	725	730	735	740	745	750	755	
242	ata gga	gac ctc	agt gcc	atc gat	gaa acc cca	atc atg	gac tca	acc
243	Ile Gly	Asp Leu	Ser Ala	Ile Asp	Glu Thr	Pro Ile	Met Asp	Ser Thr
244	740	745	750	755	760	765	770	
246	att tcc	act gca	acc aca	gcc ctt	gct ttg	caa gcc	agg aga	aac ccg
247	Ile Ser	Thr Ala	Thr Thr	Ala Leu	Ala Leu	Gln Ala	Arg Arg	Asn Pro
248	755	760	765	770	775	780	785	
250	gca ggg	acc aaa	tgg atg	gag cac	gta aaa cta	gaa agg cta	aaa caa	
251	Ala Gly	Thr Lys	Trp Met	Glu His	Val Lys	Leu Glu	Arg Leu	Lys Gln
252	770	775	780	785	790	795	800	
254	gtg aat	gga atg	ttt ccg	cga ctg	aac ccc	att cta	ccc cct	aaa gcc
255	Val Asn	Gly Met	Phe Pro	Arg Leu	Asn Pro	Ile Leu	Pro Pro	Lys Ala
256	790	795	800	805	810	815	820	
258	cct gcg	gtc tct	cct ctc	ata gga	aat ggc	aca cag	tcc aac	acc
259	Pro Ala	Val Ser	Pro Leu	Ile Gly	Asn Gly	Thr Gln	Ser Asn	Asn Thr
260	805	810	815	820	825	830	835	
262	tgc agc	ttg ggt	ggg ccc	atg acg	ctt ctc	ccg ggc	aga agc	gac ctc
263	Cys Ser	Leu Gly	Gly Pro	Met Thr	Leu Leu	Pro Gly	Arg Ser	Asp Leu
264	820	825	830	835	840	845	850	
266	tct ggg	gtg gac	gtc act	atg ctg	aac atg	ctc aac	aga agg	gac agc
267	Ser Gly	Val Asp	Val Thr	Met Leu	Asn Met	Leu Asn	Arg Arg	Asp Ser
268	835	840	845	850	855	860	865	

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270	agc	gcc	agc	acc	atc	agc	tcg	gcc	tac	ctg	agc	agc	cgc	cgc	tcc	tca	2649
271	Ser	Ala	Ser	Thr	Ile	Ser	Ser	Ala	Tyr	Leu	Ser	Ser	Arg	Arg	Ser	Ser	
272	850				855					860						865	
274	ggg	atc	tcg	ccc	tgc	ttc	tcc	agc	cgc	cgc	tcc	agc	gag	gag	tca	cag	2697
275	Gly	Ile	Ser	Pro	Cys	Phe	Ser	Ser	Arg	Arg	Ser	Ser	Glu	Ala	Ser	Gln	
276						870				875						880	
278	gcc	gag	ggc	cgg	ccg	cag	aac	gtg	agc	gtg	gcc	gac	tcc	tac	gac	ccc	2745
279	Ala	Glu	Gly	Arg	Pro	Gln	Asn	Val	Ser	Val	Ala	Asp	Ser	Tyr	Asp	Pro	
280						885				890						895	
282	atc	tcc	acc	gac	gcc	tcg	cgc	cgc	tcc	agc	gaa	gcc	agc	cag	agc	gac	2793
283	Ile	Ser	Thr	Asp	Ala	Ser	Arg	Arg	Ser	Ser	Glu	Ala	Ser	Gln	Ser	Asp	
284						900				905						910	
286	ggc	ctg	ccc	agc	ctg	ctc	agc	ctc	ccc	gcc	cag	cag	tac	cgc	ctc		2841
287	Gly	Leu	Pro	Ser	Leu	Leu	Ser	Leu	Thr	Pro	Ala	Gln	Gln	Tyr	Arg	Leu	
288						915				920						925	
290	aag	gcc	aag	tac	gac	gct	gcc	aca	gga	ggg	ccg	ccg	ccg	acg	.ccc	ctg	2889
291	Lys	Ala	Lys	Tyr	Ala	Ala	Ala	Thr	Gly	Gly	Pro	Pro	Pro	Pro	Thr	Pro	Leu
292						930				935						940	
294	ccc	aac	atg	gag	agg	atg	agc	ctg	aag	acg	cgc	ctg	gcf	ctc	ggg		2937
295	Pro	Asn	Met	Glu	Arg	Met	Ser	Leu	Lys	Thr	Arg	Leu	Ala	Leu	Gly		
296						950				955						960	
298	gat	gcc	ctc	gag	cct	ggc	gtg	gcc	ctg	cct	cca	gtt	cat	gcc	ccg	agg	2985
299	Asp	Ala	Leu	Glu	Pro	Gly	Val	Ala	Leu	Pro	Pro	Val	His	Ala	Pro	Arg	
300						965				970						975	
302	agg	tgc	agc	gac	ggg	gga	gcc	cac	ggc	tac	ggg	ccg	cgc	cac	ctg	cag	3033
303	Arg	Cys	Ser	Asp	Gly	Gly	Ala	His	Gly	Tyr	Gly	Arg	Arg	His	Leu	Gln	
304						980				985						990	
306	ccg	cac	gat	gcf	ctg	ggc	cac	ggc	gtg	agg	agg	gcc	agc	gac	ccg	gtg	3081
307	Pro	His	Asp	Ala	Leu	Gly	His	Gly	Val	Arg	Arg	Ala	Ser	Asp	Pro	Val	
308						995				1000						1005	
310	cgf	aca	ggc	tcc	gag	ggc	ctg	gcc	ctg	cgt	gtg	ccg	ccg	tcc	agc		3129
311	Arg	Thr	Gly	Ser	Glu	Gly	Leu	Ala	Leu	Pro	Arg	Val	Pro	Arg	Phe	Ser	
312						1010				1015						1020	
314	agc	ctc	agc	agc	tgc	aac	ccc	ccg	atg	gcc	acg	tcc	gcf	gag	aag		3177
315	Ser	Leu	Ser	Ser	Cys	Asn	Pro	Pro	Ala	Met	Ala	Thr	Ser	Ala	Glu	Lys	
316						1030				1035						1040	
318	cgc	agt	ctc	gtt	ctt	cag	aat	tac	acg	ccg	ccc	gag	ggc	ggc	cag	tcc	3225
319	Arg	Ser	Leu	Val	Leu	Gln	Asn	Tyr	Thr	Arg	Pro	Glu	Gly	Gly	Gln	Ser	
320						1045				1050						1055	
322	cga	aac	tcc	cac	tcg	ccc	tgt	cct	ccc	agc	atc	acc	gag	aac	gtc		3273
323	Arg	Asn	Phe	His	Ser	Ser	Pro	Cys	Pro	Pro	Ser	Ile	Thr	Glu	Asn	Val	
324						1060				1065						1070	
326	acc	ctg	gag	tcc	ctg	acc	atg	gac	gct	gat	gcc	aac	ctg	aac	gat	gag	3321
327	Thr	Leu	Glu	Ser	Leu	Thr	Met	Asp	Ala	Asp	Ala	Asn	Leu	Asn	Asp	Glu	
328						1075				1080						1085	
330	gat	ttc	ctg	ccg	gac	gac	gtg	gtg	cag	tat	tta	aat	tcc	cag	aac	caa	3369
331	Asp	Phe	Leu	Pro	Asp	Asp	Val	Val	Gln	Tyr	Leu	Asn	Ser	Gln	Gln		
332						1090				1095						1100	
334	gca	ggg	tac	gag	cag	cac	tcc	ccc	agc	gcc	ctc	ccg	gac	gac	agc	aaa	3417

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date